

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

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Application Serial Number: 10/568,737
Source: IFW/P
Date Processed by STIC: 2/27/06

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

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<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

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1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
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Revised 01/10/06

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10/568,737

AMC – STIC Systems Branch – 03/02/06



IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/568,737

DATE: 02/27/2006

TIME: 15:06:53

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\02272006\J568737.raw

3 <110> APPLICANT: SHIRE BIOCHEM INC.
 5 <120> TITLE OF INVENTION: POLYPEPTIDES OF STREPTOCOCCUS PYOGENES
 7 <130> FILE REFERENCE: 51564-44
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/568,737
 C--> 10 <141> CURRENT FILING DATE: 2006-02-15
 12 <150> PRIOR APPLICATION NUMBER: US 60/495,094
 13 <151> PRIOR FILING DATE: 2003-08-15
 15 <160> NUMBER OF SEQ ID NOS: 44
 17 <170> SOFTWARE: PatentIn version 3.3
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 537
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Streptococcus pyogenes
 24 <400> SEQUENCE: 1
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 27 aacaatgta ttactgttaa aggccctaaa ggcgaactca ctctgagatt caacaaaaat 120
 29 attgaaatca aagttgaagg gactgaaatc acagttgtac gtcctaacga ctcaaaagaa 180
 31 atgaaaacaa tccatggtac aaccctgtct aacttgaata acatggttgt aggtgtttct 240
 33 gaaggtttca aaaaagatct tgaaatgaag ggtgtcggtt accgtgctca acttcaaggt 300
 35 actaaacttg tcctttcagt aggtaaatct caccaagacg aagttgaagc tccagaagga 360
 37 attactttca ctgttgctaa cccaacttca atctcagttg aaggaatcaa caaagaagtt 420
 39 gttggtcaaa cagctgctta catccgtagc ttgcgttcac cagagcctta caaaggcaaa 480
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 45 <211> LENGTH: 178
 46 <212> TYPE: PRT
 47 <213> ORGANISM: Streptococcus pyogenes
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 55 Leu Thr Asn Asn Asn Asn Val Ile Thr Val Lys Gly Pro Lys Gly Glu
 56 20 25 30
 59 Leu Thr Arg Glu Phe Asn Lys Asn Ile Glu Ile Lys Val Glu Gly Thr
 60 35 40 45
 63 Glu Ile Thr Val Val Arg Pro Asn Asp Ser Lys Glu Met Lys Thr Ile
 64 50 55 60
 67 His Gly Thr Thr Arg Ala Asn Leu Asn Asn Met Val Val Gly Val Ser
 68 65 70 75 80
 71 Glu Gly Phe Lys Lys Asp Leu Glu Met Lys Gly Val Gly Tyr Arg Ala
 72 85 90 95
 75 Gln Leu Gln Gly Thr Lys Leu Val Leu Ser Val Gly Lys Ser His Gln
 76 100 105 110
 79 Asp Glu Val Glu Ala Pro Glu Gly Ile Thr Phe Thr Val Ala Asn Pro

Does Not Comply
 Corrected Diskette Needed
 (Pg. 5)

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Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\02272006\J568737.raw

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83 Thr Ser Ile Ser Val Glu Gly Ile Asn Lys Glu Val Val Gly Gln Thr
84          130          135          140
87 Ala Ala Tyr Ile Arg Ser Leu Arg Ser Pro Glu Pro Tyr Lys Gly Lys
88 145          150          155          160
91 Gly Ile Arg Tyr Val Gly Glu Tyr Val Arg Leu Lys Glu Gly Lys Thr
92          165          170          175
95 Gly Lys
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100 <211> LENGTH: 1269
101 <212> TYPE: DNA
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109 tctagtgtca acaaagtaaa agccttaacc ataaaaagaag ccatggaaca aggaaaagat      180
111 atcagcttga ccttagctgg cgaagtaaca gctaacaaca gcagcaaagt caaaatcgac      240
113 tcaagtaaag gagaagtcaa agaggtcttt gttaaaaaag gcgatgttgt caaagtagga      300
115 caacccttgt ttagctatga aacgtcacag cgggttaacgg ctcaaagttc agaatttgat      360
117 gttcaaacca aagccaatca gtcccaagtt gctaaaacca atgcagcatt gaagtgggaa      420
119 acctacaatc gcaagggtcaa tgaaatcaac accctaaaat ctgcgtacaa cactgcacca      480
121 gatgagagct tactagagca aattcgcagc gcagaagaca gtgtatccca agcactaagc      540
123 gatgccaaaa cagcagatag cgatgtcaaa accgctcaaa tcgaactcga taaagctaata      600
125 gctactgcca caacggaaaa aggtaaacta gagtatgaca ccgttaagtc agacaccgca      660
127 ggaaccattg ttagtctaaa tactgatttg ccaaataaat caaaatccaa aaaagaaaat      720
129 gaaactttta tggaatttat cgacaaatca aaaatgttag tcaaaggtaa cattagttaa      780
131 ttgaccgtg acaagttaaa aatcgggtcaa aaagtcgaag tgattgaccg caaagacaac      840
133 tctaaaaaat ggactggaaa agtaacccaa gttggcaacc tcaaagcaga ggaaaaaggc      900
135 caagggtcaag gccaaagggtgg caatgaccaa caagataatc caaaccaagc aaaattccct      960
137 tatgttattg aacttgacca atcagacaag cagccactca ttgggtcaca cacctatgtt     1020
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141 gcagaaaaatg gaaaaaccta tgtgtggaaa gttgataaaa acaagggtcaa aaaacaagaa     1140
143 atcaagacta agcccttctc aaaaggttat gttgaggtaa caagtggctt gactatgcaa     1200
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153 <213> ORGANISM: Streptococcus pyogenes
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162          20          25          30
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166          35          40          45
169 Leu Thr Ile Lys Glu Ala Met Glu Gln Gly Lys Asp Ile Ser Leu Thr
170          50          55          60
173 Leu Ala Gly Glu Val Thr Ala Asn Asn Ser Ser Lys Val Lys Ile Asp

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174 65          70          75          80
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178          85          90          95
181 Val Lys Val Gly Gln Pro Leu Phe Ser Tyr Glu Thr Ser Gln Arg Leu
182          100          105          110
185 Thr Ala Gln Ser Ser Glu Phe Asp Val Gln Thr Lys Ala Asn Gln Leu
186          115          120          125
189 Gln Val Ala Lys Thr Asn Ala Ala Leu Lys Trp Glu Thr Tyr Asn Arg
190          130          135          140
193 Lys Val Asn Glu Ile Asn Thr Leu Lys Ser Arg Tyr Asn Thr Ala Pro
194 145          150          155          160
197 Asp Glu Ser Leu Leu Glu Gln Ile Arg Ser Ala Glu Asp Ser Val Ser
198          165          170          175
201 Gln Ala Leu Ser Asp Ala Lys Thr Ala Asp Ser Asp Val Lys Thr Ala
202          180          185          190
205 Gln Ile Glu Leu Asp Lys Ala Asn Ala Thr Ala Thr Thr Glu Lys Gly
206          195          200          205
209 Lys Leu Glu Tyr Asp Thr Val Lys Ser Asp Thr Ala Gly Thr Ile Val
210          210          215          220
213 Ser Leu Asn Thr Asp Leu Pro Asn Gln Ser Lys Ser Lys Lys Glu Asn
214 225          230          235          240
217 Glu Thr Phe Met Glu Ile Ile Asp Lys Ser Lys Met Leu Val Lys Gly
218          245          250          255
221 Asn Ile Ser Glu Phe Asp Arg Asp Lys Leu Lys Ile Gly Gln Lys Val
222          260          265          270
225 Glu Val Ile Asp Arg Lys Asp Asn Ser Lys Lys Trp Thr Gly Lys Val
226          275          280          285
229 Thr Gln Val Gly Asn Leu Lys Ala Glu Glu Lys Gly Gln Gly Gln Gly
230          290          295          300
233 Gln Gly Gly Asn Asp Gln Gln Asp Asn Pro Asn Gln Ala Lys Phe Pro
234 305          310          315          320
237 Tyr Val Ile Glu Leu Asp Gln Ser Asp Lys Gln Pro Leu Ile Gly Ser
238          325          330          335
241 His Thr Tyr Val Asn Val Leu Asn Asn Val Pro Glu Ala Gly Lys Ile
242          340          345          350
245 Val Leu Lys Glu Thr Phe Thr Met Ala Glu Asn Gly Lys Thr Tyr Val
246          355          360          365
249 Trp Lys Val Asp Lys Asn Lys Val Lys Lys Gln Glu Ile Lys Thr Lys
250          370          375          380
253 Pro Phe Ser Lys Gly Tyr Val Glu Val Thr Ser Gly Leu Thr Met Gln
254 385          390          395          400
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262          420
265 <210> SEQ ID NO: 5
266 <211> LENGTH: 885
267 <212> TYPE: DNA
268 <213> ORGANISM: Streptococcus pyogenes

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275 gttgctgtgg ttgatatctg tgaccgttta aatttagacc tcgttggggt ttgtgatagt      180
277 aaattatata cccttcctaa acgctatgat gctgttaagc gtgtgggttt acccatgaat      240
279 cctgatatag agttgattgc ttctttgaaa ccaacttgga ttttgagtcc caattcttta      300
281 caagaagatt tggaaaccaa gtatcaaaaa ttggatactg agtatggttt tttgaactta      360
283 cgaagtgttg agggcatgta ccagtccatt gatgatttag ggaacctttt ccaacgtcaa      420
285 caagaagcaa aagaattgcg ccagcaatac caggactatt atcgtgcttt ccaagctaaa      480
287 cgtaagggga agaaaaagcc taaagtgctt attcttatgg gcttgccagg tagttatttg      540
289 gtggcgacga accaatctta ttaggggaat cttttggact tggcagggtg tgagaatgtt      600
291 tatcagtcag atgagaaaga atttctatca gctaactctg aagacatgct ggctaaggag      660
293 cctgacttga ttttacgaac agctcatgcc attccagaca aggtaaaagt gatgtttgac      720
295 aaagaatttg ctgaaaatga tattttgaaa cattttacgg cagtcaagga agggaaagtc      780
297 tatgatattg acaataccct gtttggcatg agtgctaaat tgaactaccc agaagccttg      840
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303 <211> LENGTH: 294
304 <212> TYPE: PRT
305 <213> ORGANISM: Streptococcus pyogenes
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314 20 25 30
317 Gln Gln Arg Ile Val Ala Thr Ser Val Ala Val Val Asp Ile Cys Asp
318 35 40 45
321 Arg Leu Asn Leu Asp Leu Val Gly Val Cys Asp Ser Lys Leu Tyr Thr
322 50 55 60
325 Leu Pro Lys Arg Tyr Asp Ala Val Lys Arg Val Gly Leu Pro Met Asn
326 65 70 75 80
329 Pro Asp Ile Glu Leu Ile Ala Ser Leu Lys Pro Thr Trp Ile Leu Ser
330 85 90 95
333 Pro Asn Ser Leu Gln Glu Asp Leu Glu Pro Lys Tyr Gln Lys Leu Asp
334 100 105 110
337 Thr Glu Tyr Gly Phe Leu Asn Leu Arg Ser Val Glu Gly Met Tyr Gln
338 115 120 125
341 Ser Ile Asp Asp Leu Gly Asn Leu Phe Gln Arg Gln Gln Glu Ala Lys
342 130 135 140
345 Glu Leu Arg Gln Gln Tyr Gln Asp Tyr Tyr Arg Ala Phe Gln Ala Lys
346 145 150 155 160
349 Arg Lys Gly Lys Lys Lys Pro Lys Val Leu Ile Leu Met Gly Leu Pro
350 165 170 175
353 Gly Ser Tyr Leu Val Ala Thr Asn Gln Ser Tyr Val Gly Asn Leu Leu
354 180 185 190
357 Asp Leu Ala Gly Gly Glu Asn Val Tyr Gln Ser Asp Glu Lys Glu Phe
358 195 200 205
361 Leu Ser Ala Asn Pro Glu Asp Met Leu Ala Lys Glu Pro Asp Leu Ile
362 210 215 220

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365 Leu Arg Thr Ala His Ala Ile Pro Asp Lys Val Lys Val Met Phe Asp
 366 225 230 235 240
 369 Lys Glu Phe Ala Glu Asn Asp Ile Trp Lys His Phe Thr Ala Val Lys
 370 245 250 255
 373 Glu Gly Lys Val Tyr Asp Leu Asp Asn Thr Leu Phe Gly Met Ser Ala
 374 260 265 270
 377 Lys Leu Asn Tyr Pro Glu Ala Leu Asp Thr Leu Thr Gln Leu Phe Asp
 378 275 280 285
 381 His Val Gly Asp His Pro
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 386 <211> LENGTH: 34
 387 <212> TYPE: DNA
 388 <213> ORGANISM: Primer
 390 <400> SEQUENCE: 7
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 395 <211> LENGTH: 29
 396 <212> TYPE: DNA
 397 <213> ORGANISM: Primer
 399 <400> SEQUENCE: 8
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 406 <213> ORGANISM: Primer
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 423 <212> TYPE: DNA
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 433 <213> ORGANISM: Primer
 435 <400> SEQUENCE: 12
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 439 <210> SEQ ID NO: 13
 440 <211> LENGTH: 30
 441 <212> TYPE: DNA

The type of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/568,737

DATE: 02/27/2006

TIME: 15:06:54

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\02272006\J568737.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date